Schnitzer

1632

Serial Number: 08/973,363

CRF Processing Date: 1/18/2000
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically ~~ENTERED~~

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☑ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: moved (iv) CORRES. ADDRESS: section up a few line
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/973,363*

DATE: 01/18/2000
TIME: 14:03:25

INPUT SET: S34486.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4         (i) APPLICANT:
 5              (A) NAME: GRIFFITHS, RICHARD
 6              (B) STREET: 20 (TR) Woodcroft Avenue, Broomhill,
 7              (C) CITY: Glasgow
 8              (E) COUNTRY: United Kingdom
 9              (F) POSTAL CODE (ZIP): G11 7HX
10
11              (A) NAME: TIWARI, BELA
12              (B) STREET: 4 Upway Road
13              (C) CITY: Oxford
14              (E) COUNTRY: United Kingdom
15              (F) POSTAL CODE (ZIP): OX3 9QH
16         (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
17    SEX IDENTIFICATION IN BIRDS
18         (iii) NUMBER OF SEQUENCES: 39
19         (iv) CORRESPONDENCE ADDRESS:
20              (A) ADDRESSEE:  WENDEROTH, LIND & PONACK, L.L.P.
21              (B) STREET: 2033 K. Street, N.W., Suite 800,
22              (C) CITY:  Washington
23              (D) STATE: D.C.
24              (E) COUNTRY:  U.S.A.
25              (F) ZIP:  20006
26         (v) COMPUTER READABLE FORM:
27              (A) MEDIUM TYPE: Floppy disk
28              (B) COMPUTER: IBM PC compatible
29              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
31         (vi) CURRENT APPLICATION DATA:
32              (A) APPLICATION NUMBER:
33              (B) FILING DATE:
34         (vii) PRIOR APPLICATION DATA:
35              (A) APPLICATION NUMBER: WO PCT/GB96/01341
36              (B) FILING DATE:05-JUN-1996
37         (vii) PRIOR APPLICATION DATA:
38              (A) APPLICATION NUMBER: GB 9511439.3
39              (B) FILING DATE:06-JUN-1995
40         (viii) ATTORNEY/AGENT INFORMATION:
41              (A) NAME: Warren M Cheek, Jr.
42              (B) REGISTRATION NUMBER:  33,367
43              (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US
44         (ix) TELECOMMUNICATION INFORMATION:
45              (A) TELEPHONE:  (202)-721-8200
46              (B) TELEFAX:  (202)-721-8250
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INPUT SET: S34486.raw

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47              (C) TELEX:
48    (2) INFORMATION FOR SEQ ID NO: 1:
49        (i) SEQUENCE CHARACTERISTICS:
50            (A) LENGTH: 723 base pairs
51            (B) TYPE: nucleic acid
52            (C) STRANDEDNESS: double
53            (D) TOPOLOGY: linear
54       (ii) MOLECULE TYPE: DNA (genomic)
55       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
56    CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC    60
57    AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT   120
58    AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTGA GCGAAGTTTG TTTGGGGATT   180
59    TTAGTTTGGT TTCCCTGTCA CTGTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG   240
60    AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA   300
61    CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG   360
62    ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC   420
63    ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA   480
64    TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG   540
65    ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT   600
66    CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA   660
67    GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC   720
68    GGG                                                              723
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70    (2) INFORMATION FOR SEQ ID NO: 2:
71        (i) SEQUENCE CHARACTERISTICS:
72            (A) LENGTH: 153 base pairs
73            (B) TYPE: nucleic acid
74            (C) STRANDEDNESS: double
75            (D) TOPOLOGY: linear
76       (ii) MOLECULE TYPE: cDNA
77
78       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
79    ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAAACCA    60
80    CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT   120
81    GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG                               153
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84        (i) SEQUENCE CHARACTERISTICS:
85            (A) LENGTH: 153 base pairs
86            (B) TYPE: nucleic acid
87            (C) STRANDEDNESS: double
88            (D) TOPOLOGY: linear
89       (ii) MOLECULE TYPE: cDNA
90       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
91    ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC    60
92    CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT   120
93    GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA                               153
94    (2) INFORMATION FOR SEQ ID NO: 4:
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96        (i) SEQUENCE CHARACTERISTICS:
97            (A) LENGTH: 153 base pairs
98            (B) TYPE: nucleic acid
99            (C) STRANDEDNESS: double
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100              (D) TOPOLOGY: linear
101          (ii) MOLECULE TYPE: cDNA
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106    GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA                                    153
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108    (2) INFORMATION FOR SEQ ID NO: 5:
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110              (A) LENGTH: 153 base pairs
111              (B) TYPE: nucleic acid
112              (C) STRANDEDNESS: double
113              (D) TOPOLOGY: linear
114          (ii) MOLECULE TYPE: cDNA
115          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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117    CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT       120
118    GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA                                    153
119
120    (2) INFORMATION FOR SEQ ID NO: 6:
121          (i) SEQUENCE CHARACTERISTICS:
122              (A) LENGTH: 41 amino acids
123              (B) TYPE: amino acid
124              (C) STRANDEDNESS:
125              (D) TOPOLOGY: linear
126          (ii) MOLECULE TYPE: peptide
127          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
128    Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
129    1               5                   10                  15
130    Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys
131                20                  25                  30
132    Arg Glu Ala Gln Arg Leu Cys Gly Ala
133            35                  40
134
135    (2) INFORMATION FOR SEQ ID NO: 7:
136          (i) SEQUENCE CHARACTERISTICS:
137              (A) LENGTH: 41 amino acids
138              (B) TYPE: amino acid
139              (C) STRANDEDNESS:
140              (D) TOPOLOGY: linear
141          (ii) MOLECULE TYPE: peptide
142          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
143    Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
144    1               5                   10                  15
145    Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
146                20                  25                  30
147    Lys Glu Ala Gln Arg Leu Ala Gly Ala
148            35                  40
149
150    (2) INFORMATION FOR SEQ ID NO: 8:
151          (i) SEQUENCE CHARACTERISTICS:
152              (A) LENGTH: 41 amino acids
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153              (B) TYPE: amino acid
154              (C) STRANDEDNESS:
155              (D) TOPOLOGY: linear
156         (ii) MOLECULE TYPE: peptide
157         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
158         Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
159         1               5                   10                  15·
160         Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
161                     20                  25                  30
162         Lys Glu Ala Gln Arg Leu Ala Gly Ala
163                 35                  40
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165    (2). INFORMATION FOR SEQ ID NO: 9:
166         (i) SEQUENCE CHARACTERISTICS:
167              (A) LENGTH: 41 amino acids
168              (B) TYPE: amino acid
169              (C) STRANDEDNESS:
170              (D) TOPOLOGY: linear
171         (ii) MOLECULE TYPE: peptide
172         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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174         1               5                   10                  15
175         Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
176                     20                  25                  30
177         Lys Glu Val Gln Arg Leu Thr Gly Ala
178                 35                  40
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180    (2) INFORMATION FOR SEQ ID NO: 10:
181         (i) SEQUENCE CHARACTERISTICS:
182              (A) LENGTH: 6608 base pairs
183              (B) TYPE: nucleic acid
184              (C) STRANDEDNESS: double
185              (D) TOPOLOGY: linear
186         (ii) MOLECULE TYPE: cDNA
187         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
188    CGGGCTGCGG CACGCAGCGG ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC        60
189    CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG       120
190    CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC       180
191    ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA       240
192    GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG       300
193    GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA       360
194    GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG       420
195    AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT       480
196    CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA       540
197    AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA       600
198    GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAG CATAAAGATG        660
199    AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG       720
200    CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA       780
201    AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG       840
202    GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG       900
203    ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA       960
204    CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG      1020
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INPUT SET: S34486.raw

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206   AAGATGAATT TGAAACTATA GAGAAGTTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA   1080
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208   AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA   1200
209   TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA   1260
210   AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC   1320
211   CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT   1380
212   ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG   1440
213   ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC   1500
214   TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT CAATCCAAGA   1560
215   CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC AAGATTTGTT GCACTGAAGA   1620
216   AGCAACCATC TTACATTGGA GGACATGAAA GTCTGGAGTT AAGAGATTAT CAGTTAAATG   1680
217   GATTGAATTG GCTCGCTCAT TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA   1740
218   TGGGTCTGGG TAAAACAATA CAAACAATTT CTTTTCTGAA CTACCTGTTT CATGAACATC   1800
219   AACTGTATGG CCCTTTTCTT CTGCGCGTGC CACTTTCTAC CTTGACATCT TGGCAAAGAG   1860
220   AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA CTTAGGAGAT ATAACTAGTA   1920
221   GAAATATGAT AAGGACTCAT GAATGGATGC ATCCACAGAC TAAACGATTA AAGTTTAACA   1980
222   TACTTCTGAC GACATATGAA ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT   2040
223   GGGCATTCAT AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA   2100
224   GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC CCACTGCAAA   2160
225   ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTCATCAT GCCAGAAAAA TTTTCCTCCT   2220
226   GGGAAGATTT TGAAGAGGAG CATGGCAAAG GAAGAGAGTA TGGTTATGCA AGTCTTCACA   2280
227   AAGAGCTTGA ACCATTTTTA CTAAGAAGAG TTAAAAAAGA TGTAGAAAAG TCTTTACCTG   2340
228   CTAAGGTTGA ACAAATTCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT   2400
229   GGATTTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTC AAAAGGCAGT ACCTCAGGCT   2460
230   TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTAACCA TTGCTACCTC ATTAAGCCAC   2520
231
232   CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG   2580
233   GGAAACTAAT CCTTCTTGAC AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC   2640
234   TGATTTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC   2700
235   AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG   2760
236   ATCATTTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT ACTGTCTACA AGAGCTGGAG   2820
237   GATTAGGTAT TAACTTGGCA TCTGCTGACA CTGTAGTTAT TTTTGATTCT GACTGGAATC   2880
238   CACAGAATGA TCTGCAGGCA CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA   2940
239   ATATTTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA   3000
240   AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA AAAACTGTTC   3060
241   TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA TAAAGAAGAG TTATCAGCTA   3120
242   TTTTGAAGTT TGGTGCTGAG GAACTCTTTA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC   3180
243   AGGAAATGGA TATAGATGAA ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC   3240
244   CATTGACTGT AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG   3300
245   ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA GAAATCATCC   3360
246   CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT   3420
247   ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA   3480
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Schnizer

1632

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

Does Not Comply
Corrected Diskette Needed

```
      1                                     SEQUENCE LISTING
      2
      3    (1)    General Information:
-->   4           (i) APPLICANT:
-->   5               (A) NAME: GRIFFITHS, RICHARD
-->   6               (B) STREET: 20 (TR) Woodcroft Avenue, Broomhill,
-->   7               (C) CITY: Glasgow
-->   8               (E) COUNTRY: United Kingdom
-->   9               (F) POSTAL CODE (ZIP): G11 7HX
     10
-->  11               (A) NAME: TIWARI, BELA
-->  12               (B) STREET: 4 Upway Road
-->  13               (C) CITY: Oxford
-->  14               (E) COUNTRY: United Kingdom
-->  15               (F) POSTAL CODE (ZIP): OX3 9QH
     16          (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
     17    SEX IDENTIFICATION IN BIRDS
     18          (iii) NUMBER OF SEQUENCES: 39
     19          (iv) COMPUTER READABLE FORM:
     20               (A) MEDIUM TYPE: Floppy disk
     21               (B) COMPUTER: IBM PC compatible
     22               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     23               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
     24    (vi) CURRENT APPLICATION DATA: ← add heading
     25    (vii) (vi) PRIOR APPLICATION DATA:
     26               (A) APPLICATION NUMBER: WO PCT/GB96/01341
     27               (B) FILING DATE:05-JUN-1996
     28    (viii) (vi) PRIOR APPLICATION DATA:
     29               (A) APPLICATION NUMBER: GB 9511439.3
     30               (B) FILING DATE:06-JUN-1995
     31    (iv) (vii) CORRESPONDENCE ADDRESS:
     32               (A) ADDRESSEE:  WENDEROTH, LIND & PONACK, L.L.P.
     33               (B) STREET: 2033 K. Street, N.W., Suite 800,
     34               (C) CITY:  Washington
     35               (D) STATE: D.C.
     36               (E) COUNTRY:  U.S.A.
     37               (F) ZIP:  20006
     38    (viii) ATTORNEY/AGENT INFORMATION:
     39               (A) NAME: Warren M Cheek, Jr.
     40               (B) REGISTRATION NUMBER:  33,367
     41               (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US
     42      (ix) TELECOMMUNICATION INFORMATION:
     43               (A) TELEPHONE:  (202)-721-8200
     44               (B) TELEFAX:  (202)-721-8250
     45               (C) TELEX:
     46    (2) INFORMATION FOR SEQ ID NO: 1:
```

INPUT SET: S34486.raw

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47          (i) SEQUENCE CHARACTERISTICS:
48              (A) LENGTH: 723 base pairs
49              (B) TYPE: nucleic acid
50              (C) STRANDEDNESS: double
51              (D) TOPOLOGY: linear
52         (ii) MOLECULE TYPE: DNA (genomic)
53         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
54   CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC      60
55   AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT     120
56   AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTGA GCGAAGTTTG TTTGGGGATT     180
57   TTAGTTTGGT TTCCCTGTCA CTGTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG     240
58   AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA     300
59   CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG     360
60   ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC     420
61   ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA     480
62   TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG     540
63   ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT     600
64   CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA     660
65   GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC     720
66   GGG                                                                    723
67
68   (2) INFORMATION FOR SEQ ID NO: 2:
69          (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH: 153 base pairs
71              (B) TYPE: nucleic acid
72              (C) STRANDEDNESS: double
73              (D) TOPOLOGY: linear
74         (ii) MOLECULE TYPE: cDNA
75
76         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
77   ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAACCA      60
78   CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT     120
79   GCAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG                                    153
80
81   (2) INFORMATION FOR SEQ ID NO: 3:
82          (i) SEQUENCE CHARACTERISTICS:
83              (A) LENGTH: 153 base pairs
84              (B) TYPE: nucleic acid
85              (C) STRANDEDNESS: double
86              (D) TOPOLOGY: linear
87         (ii) MOLECULE TYPE: cDNA
88         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89   ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC      60
90   CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT     120
91   GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA                                    153
92   (2) INFORMATION FOR SEQ ID NO: 4:
93
94          (i) SEQUENCE CHARACTERISTICS:
95              (A) LENGTH: 153 base pairs
96              (B) TYPE: nucleic acid
97              (C) STRANDEDNESS: double
98              (D) TOPOLOGY: linear
99         (ii) MOLECULE TYPE: cDNA
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/973,363*

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100        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
101
102   ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC         60
103   CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT        120
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105
106   (2) INFORMATION FOR SEQ ID NO: 5:
107        (i) SEQUENCE CHARACTERISTICS:
108            (A) LENGTH: 153 base pairs
109            (B) TYPE: nucleic acid
110            (C) STRANDEDNESS: double
111            (D) TOPOLOGY: linear
112        (ii) MOLECULE TYPE: cDNA
113        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
114   ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA         60
115   CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT        120
116   GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA                                    153
117
118   (2) INFORMATION FOR SEQ ID NO: 6:
119        (i) SEQUENCE CHARACTERISTICS:
120            (A) LENGTH: 41 amino acids
121            (B) TYPE: amino acid
122            (C) STRANDEDNESS:
123            (D) TOPOLOGY: linear
124        (ii) MOLECULE TYPE: peptide
125        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
126        Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
127        1               5                   10                  15
128        Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys
129                    20                  25                  30
130        Arg Glu Ala Gln Arg Leu Cys Gly Ala
131                    35                  40
132
133   (2) INFORMATION FOR SEQ ID NO: 7:
134        (i) SEQUENCE CHARACTERISTICS:
135            (A) LENGTH: 41 amino acids
136            (B) TYPE: amino acid
137            (C) STRANDEDNESS:
138            (D) TOPOLOGY: linear
139        (ii) MOLECULE TYPE: peptide
140        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
141        Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
142        1               5                   10                  15
143        Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
144                    20                  25                  30
145        Lys Glu Ala Gln Arg Leu Ala Gly Ala
146                    35                  40
147
148   (2) INFORMATION FOR SEQ ID NO: 8:
149        (i) SEQUENCE CHARACTERISTICS:
150            (A) LENGTH: 41 amino acids
151            (B) TYPE: amino acid
152            (C) STRANDEDNESS:
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RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/973,363

INPUT SET: S34486.raw

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153              (D) TOPOLOGY: linear
154         (ii) MOLECULE TYPE: peptide
155         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
156          Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
157          1               5                   10                  15
158          Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
159                      20                  25                  30
160          Lys Glu Ala Gln Arg Leu Ala Gly Ala
161                      35                  40
162
163    (2) INFORMATION FOR SEQ ID NO: 9:
164         (i) SEQUENCE CHARACTERISTICS:
165              (A) LENGTH: 41 amino acids
166              (B) TYPE: amino acid
167              (C) STRANDEDNESS:
168              (D) TOPOLOGY: linear
169         (ii) MOLECULE TYPE: peptide
170         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
171          Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
172          1               5                   10                  15
173          Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
174                      20                  25                  30
175          Lys Glu Val Gln Arg Leu Thr Gly Ala
176                      35                  40
177
178    (2) INFORMATION FOR SEQ ID NO: 10:
179         (i) SEQUENCE CHARACTERISTICS:
180              (A) LENGTH: 6608 base pairs
181              (B) TYPE: nucleic acid
182              (C) STRANDEDNESS: double
183              (D) TOPOLOGY: linear
184         (ii) MOLECULE TYPE: cDNA
185         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
186    CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC        60
187    CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG       120
188    CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC       180
189    ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA       240
190    GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG       300
191    GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA       360
192    GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG       420
193    AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT       480
194    CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA       540
195    AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA       600
196    GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG       660
197    AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG       720
198    CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA       780
199    AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG       840
200    GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG       900
201    ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA       960
202    CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG      1020
203
204    AAGATGAATT TGAAACTATA GAGAAGTTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA      1080
205    CTGGTGCCTC AACCACCATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG      1140
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206   AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA   1200
207   TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA   1260
208   AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC   1320
209   CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT   1380
210   ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG   1440
211   ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC   1500
212   TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT CAATCCAAGA   1560
213   CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC AAGATTTGTT GCACTGAAGA   1620
214   AGCAACCATC TTACATTGGA GGACATGAAA GTCTGGAGTT AAGAGATTAT CAGTTAAATG   1680
215   GATTGAATTG GCTCGCTCAT TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA   1740
216   TGGGTCTGGG TAAAACAATA CAAACAATTT CTTTTCTGAA CTACCTGTTT CATGAACATC   1800
217   AACTGTATGG CCCTTTTCTT CTGCGCGTGC CACTTTCTAC CTTGACATCT TGGCAAAGAG   1860
218   AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA CTTAGGAGAT ATAACTAGTA   1920
219   GAAATATGAT AAGGACTCAT GAATGGATGC ATCCACAGAC TAAACGATTA AAGTTTAACA   1980
220   TACTTCTGAC GACATATGAA ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT   2040
221   GGGCATTCAT AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA   2100
222   GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC CCACTGCAAA   2160
223   ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTCATCAT GCCAGAAAAA TTTTCCTCCT   2220
224   GGGAAGATTT TGAAGAGGAG CATGGCAAAG GAAGAGAGTA TGGTTATGCA AGTCTTCACA   2280
225   AAGAGCTTGA ACCATTTTTA CTAAGAAGAG TTAAAAAAGA TGTAGAAAAG TCTTTACCTG   2340
226   CTAAGGTTGA ACAAATTCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT   2400
227   GGATTTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTC AAAAGGCAGT ACCTCAGGCT   2460
228   TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTAACCA TTGCTACCTC ATTAAGCCAC   2520
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230   CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG   2580
231   GGAAACTAAT CCTTCTTGAC AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC   2640
232   TGATTTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC   2700
233   AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG   2760
234   ATCATTTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT ACTGTCTACA AGAGCTGGAG   2820
235   GATTAGGTAT TAACTTGGCA TCTGCTGACA CTGTAGTTAT TTTTGATTCT GACTGGAATC   2880
236   CACAGAATGA TCTGCAGGCA CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA   2940
237   ATATTTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA   3000
238   AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA AAAACTGTTC   3060
239   TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA TAAAGAAGAG TTATCAGCTA   3120
240   TTTTGAAGTT TGGTGCTGAG GAACTCTTTA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC   3180
241   AGGAAATGGA TATAGATGAA ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC   3240
242   CATTGACTGT AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG   3300
243   ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA GAAATCATCC   3360
244   CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT   3420
245   ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA   3480
246   GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC   3540
247   GGCCAAAAAA GCGTGAAGGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG   3600
248   ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT   3660
249   TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC TGAGACAGAC CTTAGACGTT   3720
250   TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG   3780
251   AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC   3840
252   AGGTGAATGC AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACTG CACAAATCCA   3900
253   TTCCTTCAGA TCCAGAAGAA AGGAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC   3960
254   ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT   4020
255
256   ATGGCTATGG CAGCTGGGAA ATGATAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA   4080
257   TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT   4140
258   ACCTCATTAA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG   4200
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PATENT APPLICATION   *US/08/973,363*

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APPLICATION NUMBER
FILING DATE
CLASSIFICATION
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